Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 20:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230375.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6230375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230375.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 20:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,894,795
Mapped reads	1,557,731 / 82.21%
Unmapped reads	337,064 / 17.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,989 / 1.05%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	169,633 / 8.95%
Duplication rate	8.51%
Clipped reads	777,174 / 41.02%

2.2. ACGT Content

Number/percentage of A's	27,884,076 / 27.29%
Number/percentage of C's	19,040,550 / 18.64%
Number/percentage of T's	32,104,257 / 31.42%
Number/percentage of G's	23,117,432 / 22.63%
Number/percentage of N's	18,978 / 0.02%
GC Percentage	41.26%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3652

2.4. Mapping Quality

Mean Mapping Quality	42.87

2.5. Mismatches and indels

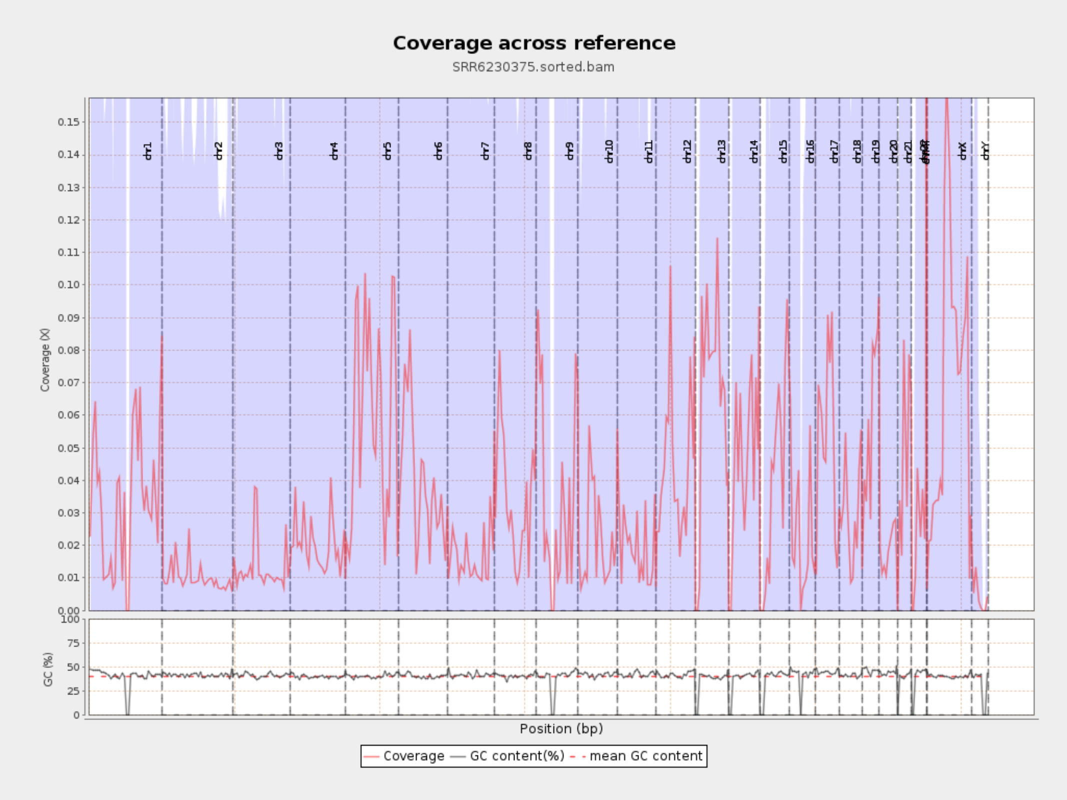
General error rate	0.91%
Mismatches	911,449
Insertions	8,158
Mapped reads with at least one insertion	0.52%
Deletions	31,067
Mapped reads with at least one deletion	1.97%
Homopolymer indels	45.85%

2.6. Chromosome stats

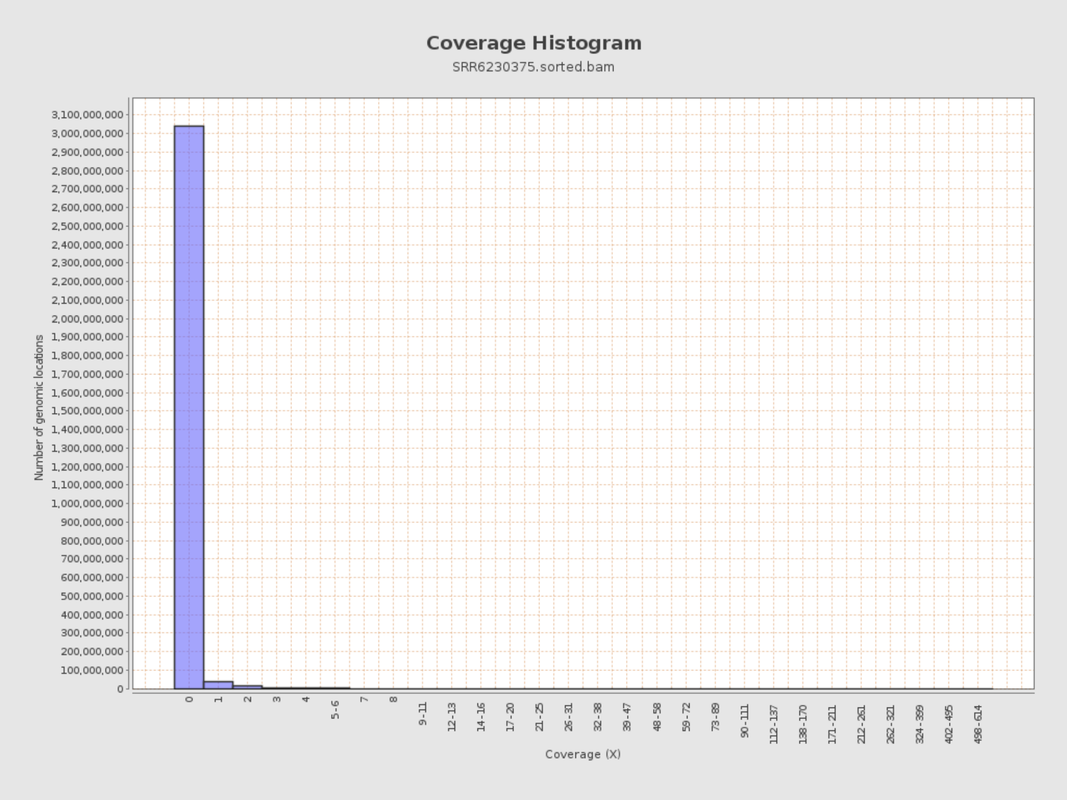
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8220180	0.033	0.5446
chr2	243199373	2458664	0.0101	0.32
chr3	198022430	2611918	0.0132	0.2063
chr4	191154276	3927240	0.0205	0.2381
chr5	180915260	10832402	0.0599	0.3982
chr6	171115067	6725263	0.0393	0.3516
chr7	159138663	2541691	0.016	0.2403

chr8	146364022	4967401	0.0339	0.4742
chr9	141213431	4667602	0.0331	0.3123
chr10	135534747	2819891	0.0208	0.3826
chr11	135006516	2830741	0.021	0.2538
chr12	133851895	5938899	0.0444	0.3435
chr13	115169878	7404707	0.0643	0.4102
chr14	107349540	4797007	0.0447	0.3572
chr15	102531392	4038233	0.0394	0.3373
chr16	90354753	2040674	0.0226	0.2494
chr17	81195210	4151641	0.0511	0.3775
chr18	78077248	2340897	0.03	0.5371
chr19	59128983	3398417	0.0575	0.4744
chr20	63025520	1175413	0.0186	0.2391
chr21	48129895	2224297	0.0462	0.3518
chr22	51304566	1135234	0.0221	0.2392
chrMT	16571	9671	0.5836	1.146
chrX	155270560	10691752	0.0689	0.4584
chrY	59373566	266930	0.0045	0.1247

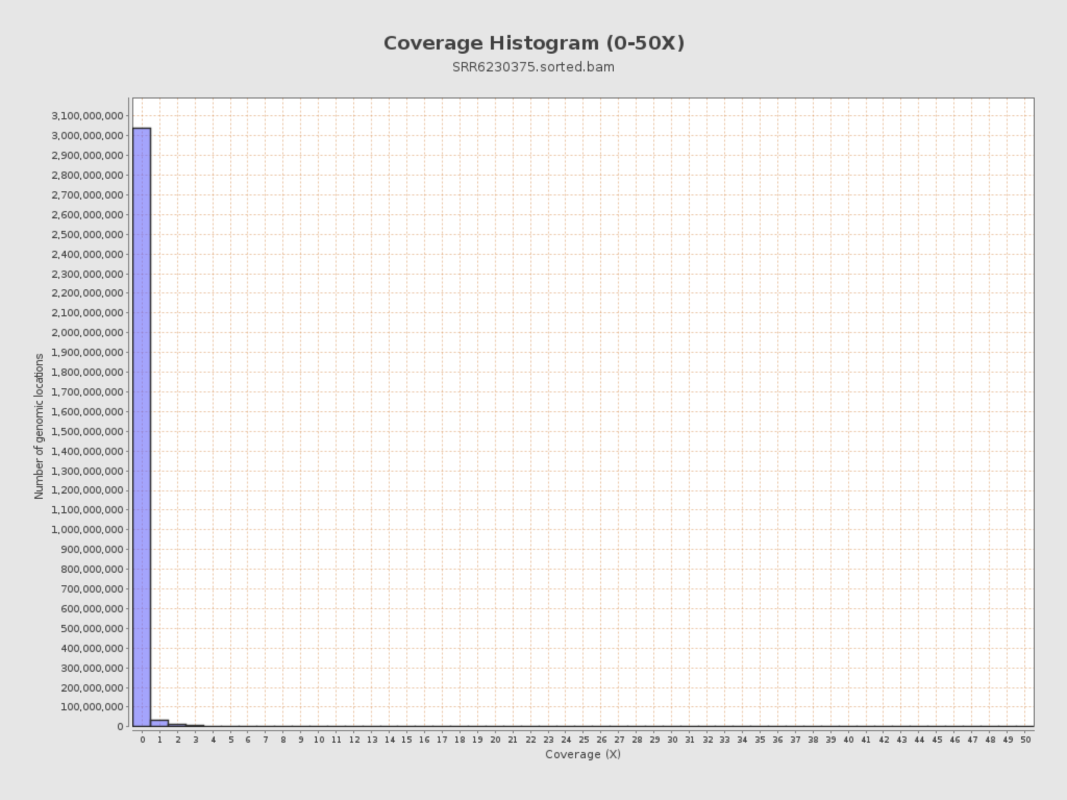
3. Results : Coverage across reference



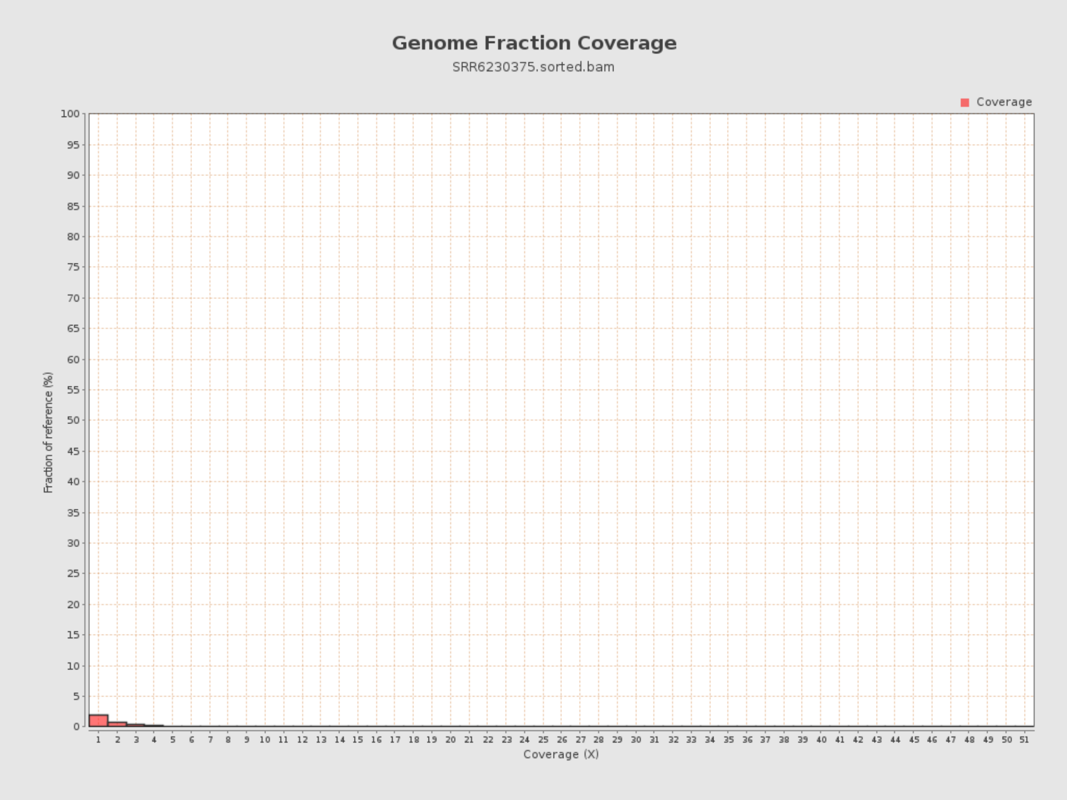
4. Results : Coverage Histogram



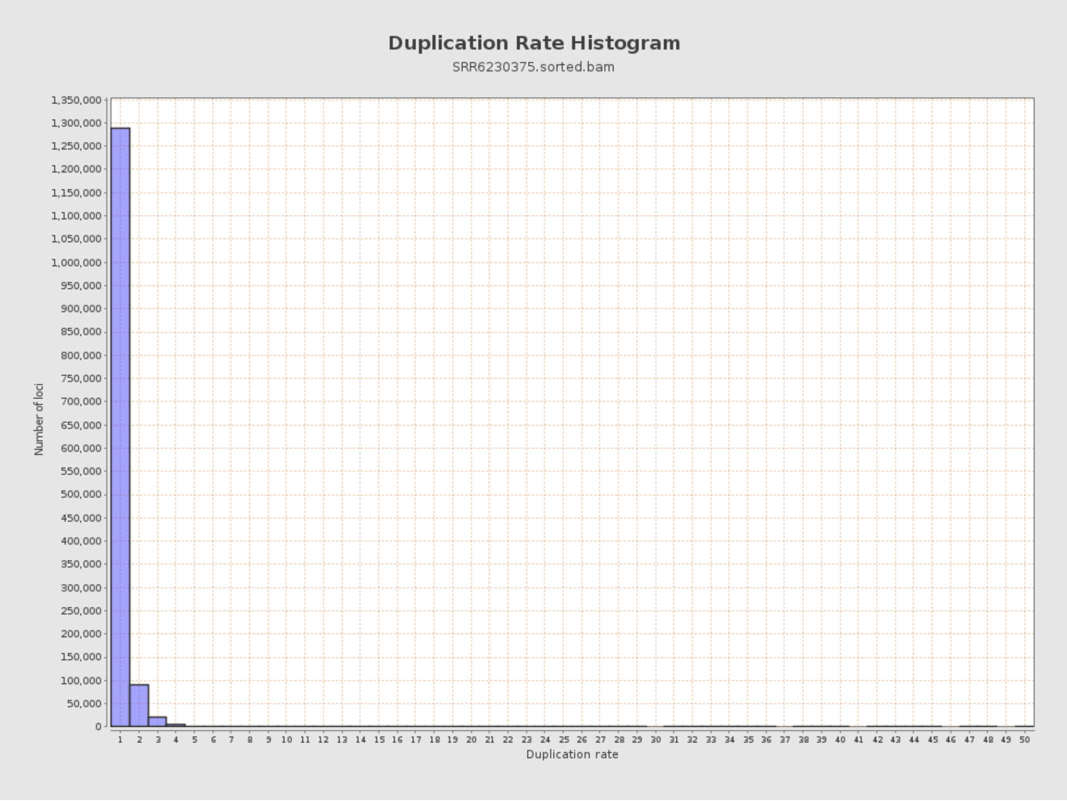
5. Results : Coverage Histogram (0-50X)



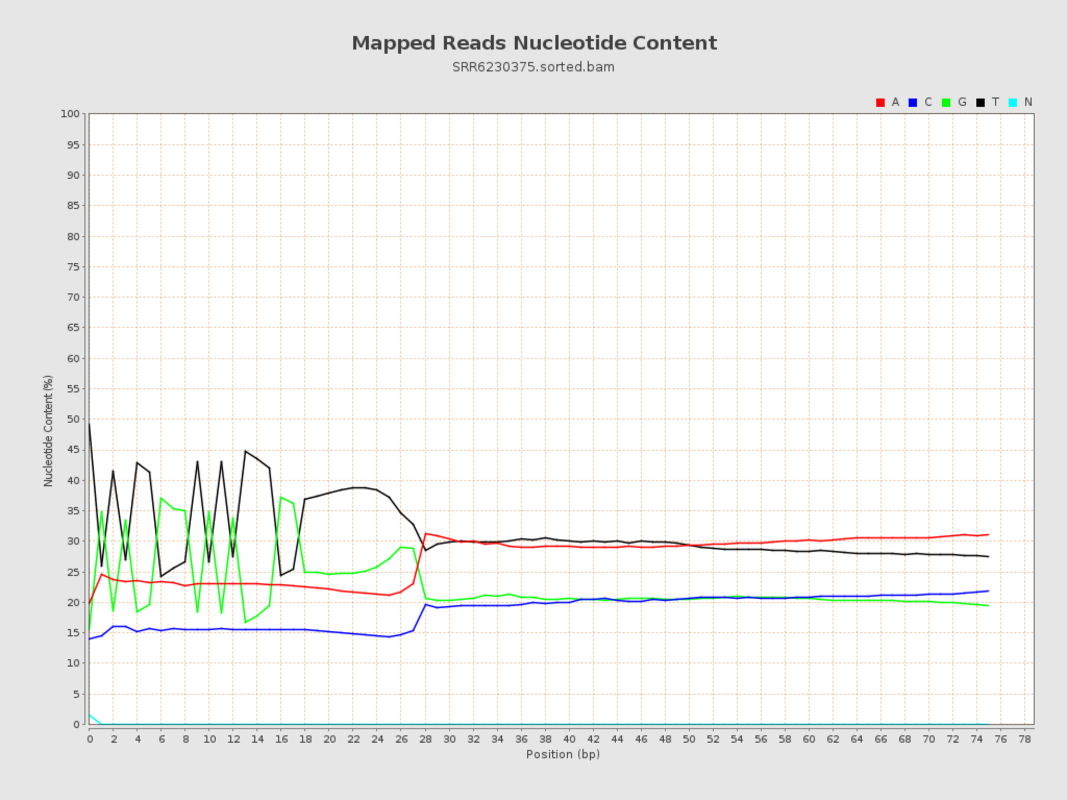
6. Results : Genome Fraction Coverage



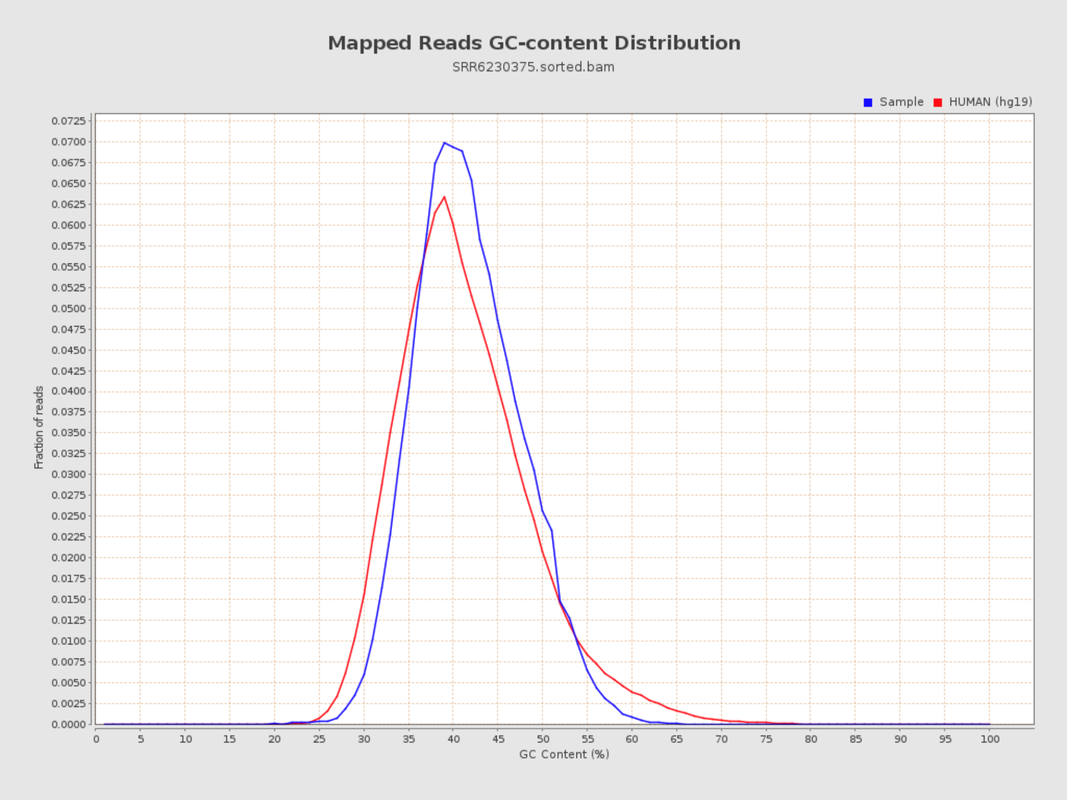
7. Results : Duplication Rate Histogram



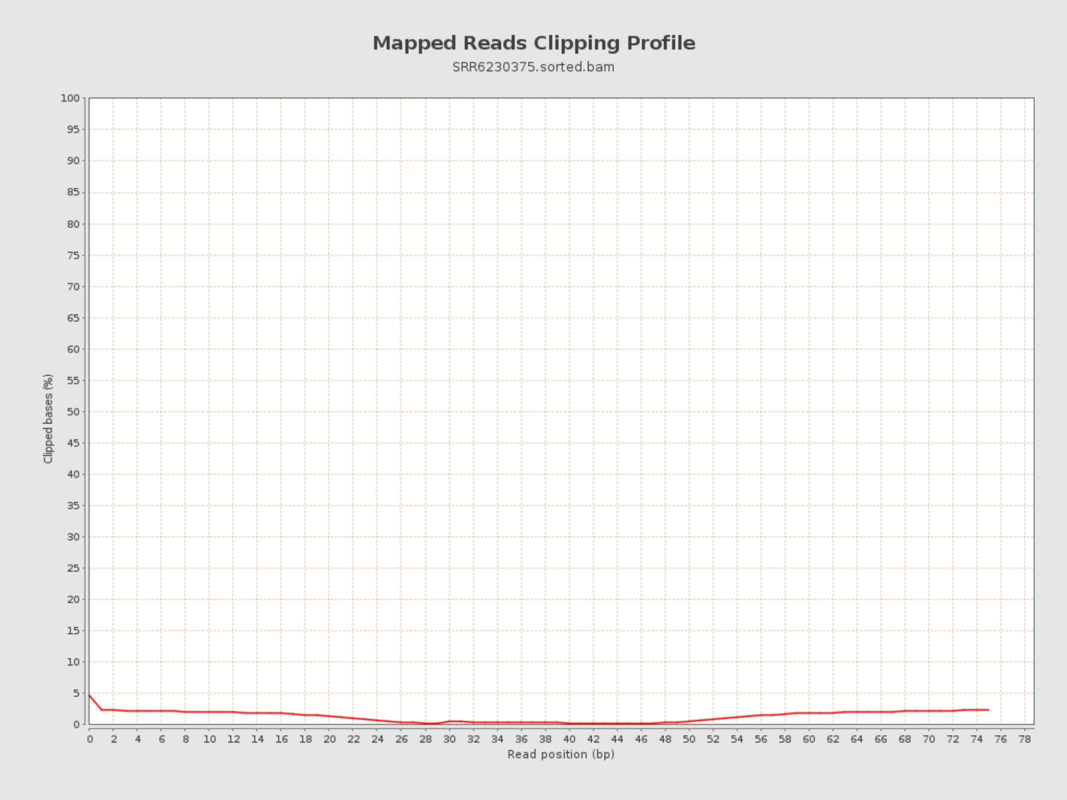
8. Results : Mapped Reads Nucleotide Content



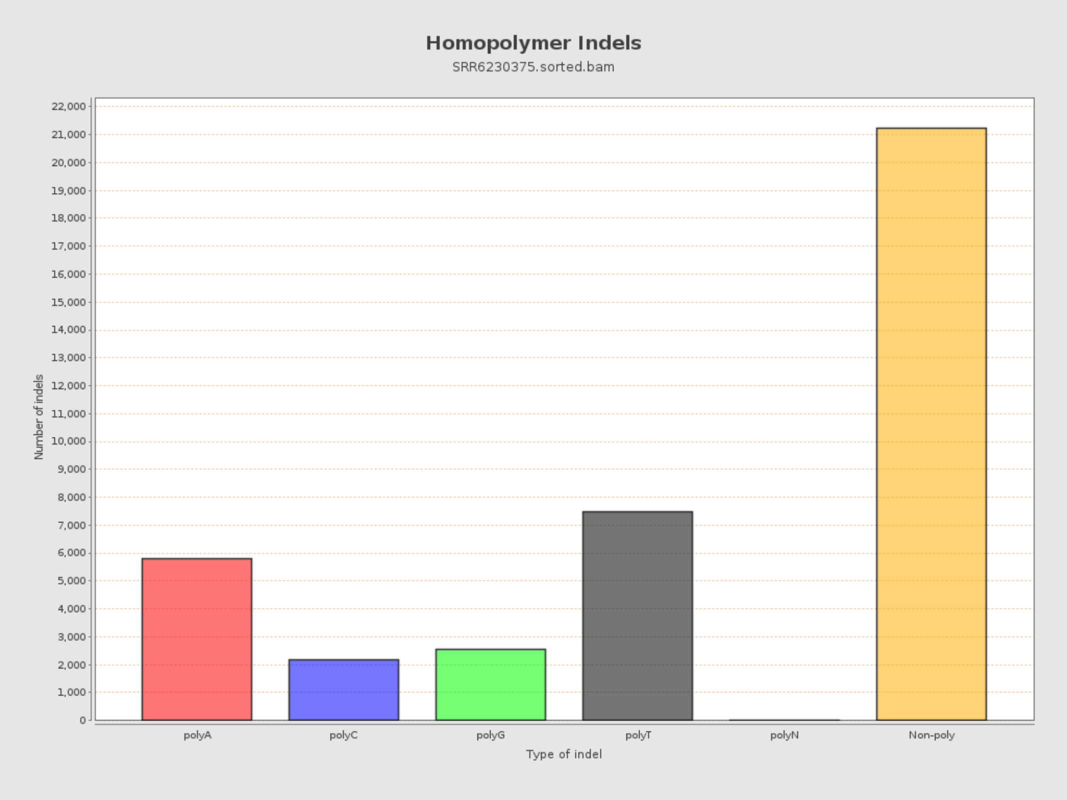
9. Results : Mapped Reads GC-content Distribution



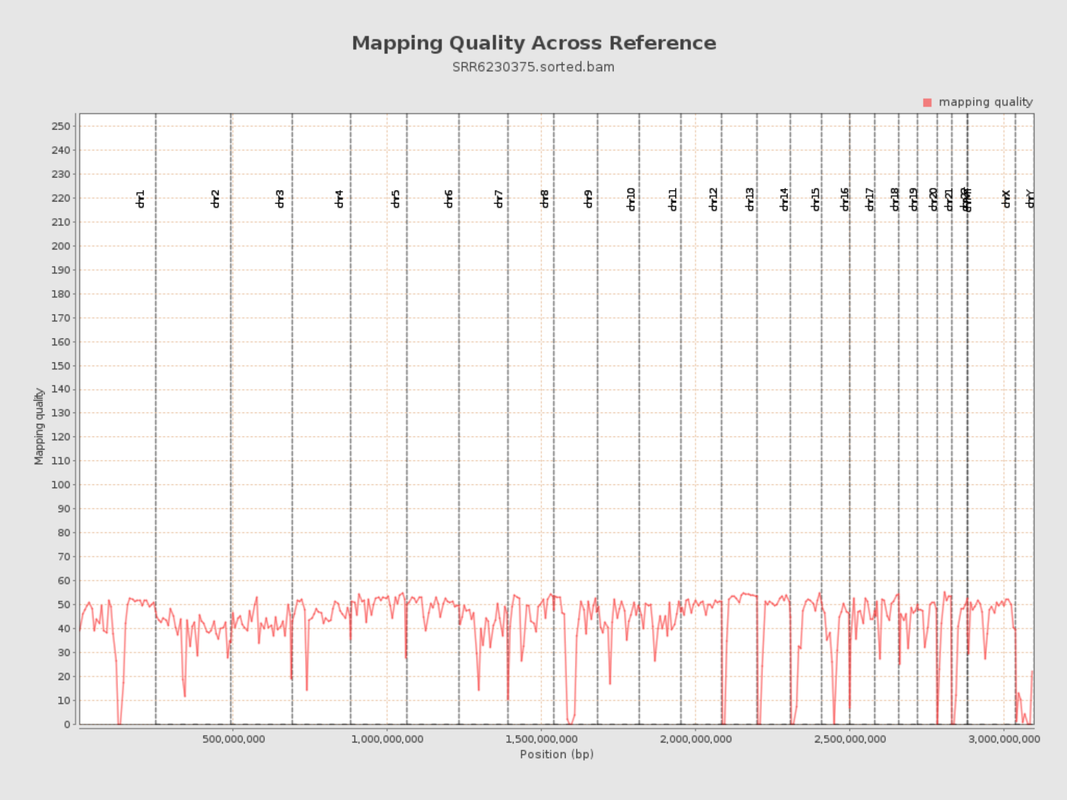
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram